



SEQUENCE LISTING

<110> Ian Popoff
Jacqueline Wyatt

<120> ANTISENSE MODULATION OF DAMAGE-SPECIFIC DNA BINDING PROTEIN 1, P127
EXPRESSION

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<141> 2000-12-06

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Met Ser Tyr Asn Tyr

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gtg gta acg gcc cag aag ccc acc gcc gtg aac ggc tgc gtg acc gga 163

Val Val Thr Ala Gln Lys Pro Thr Ala Val Asn Gly Cys Val Thr Gly

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cac ttt act tcg gcc gaa gac tta aac ctg ttg att gcc aaa aac acg 211

His Phe Thr Ser Ala Glu Asp Leu Asn Leu Leu Ile Ala Lys Asn Thr

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aga tta gag atc tat gtg gtc acc gcc gag ggg ctt cgg ccc gtc aaa 259

Arg Leu Glu Ile Tyr Val Val Thr Ala Glu Gly Leu Arg Pro Val Lys

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gag gtg ggc atg tat ggg aag att gcg gtc atg gag ctt ttc agg ccc 307

Glu Val Gly Met Tyr Gly Lys Ile Ala Val Met Glu Leu Phe Arg Pro

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aag ggg gag agc aag gac ctg ctg ttt atc ttg aca gcg aag tac aat 355

Lys	Gly	Glu	Ser	Lys	Asp	Leu	Leu	Phe	Ile	Leu	Thr	Ala	Lys	Tyr	Asn	
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Ala	Cys	Ile	Leu	Glu	Tyr	Lys	Gln	Ser	Gly	Glu	Ser	Ile	Asp	Ile	Ile	
				90					95					100		
acg	cga	gcc	cat	ggc	aat	gtc	cag	gac	cgc	att	ggc	cgc	ccc	tca	gag	451
Thr	Arg	Ala	His	Gly	Asn	Val	Gln	Asp	Arg	Ile	Gly	Arg	Pro	Ser	Glu	
			105					110					115			
acc	ggc	att	att	ggc	atc	att	gac	cct	gag	tgc	cgg	atg	att	ggc	ctg	499
Thr	Gly	Ile	Ile	Gly	Ile	Ile	Asp	Pro	Glu	Cys	Arg	Met	Ile	Gly	Leu	
		120					125					130				
cgt	ctc	tat	gat	ggc	ctt	ttc	aag	gtt	att	cca	cta	gat	cgc	gat	aat	547
Arg	Leu	Tyr	Asp	Gly	Leu	Phe	Lys	Val	Ile	Pro	Leu	Asp	Arg	Asp	Asn	
	135					140				145						
aaa	gaa	ctc	aag	gcc	ttc	aac	atc	cgc	ctg	gag	gag	ctg	cat	gtc	att	595
Lys	Glu	Leu	Lys	Ala	Phe	Asn	Ile	Arg	Leu	Glu	Glu	Leu	His	Val	Ile	
150					155				160					165		
gat	gtc	aag	ttc	cta	tat	ggt	tgc	caa	gca	cct	act	att	tgc	ttt	gtc	643
Asp	Val	Lys	Phe	Leu	Tyr	Gly	Cys	Gln	Ala	Pro	Thr	Ile	Cys	Phe	Val	
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tac	cag	gac	cct	cag	ggg	cgg	cac	gta	aaa	acc	tat	gag	gtg	tct	ctc	691
Tyr	Gln	Asp	Pro	Gln	Gly	Arg	His	Val	Lys	Thr	Tyr	Glu	Val	Ser	Leu	
			185					190				195				
cga	gaa	aag	gaa	ttc	aat	aag	ggc	cct	tgg	aaa	cag	gaa	aat	gtc	gaa	739
Arg	Glu	Lys	Glu	Phe	Asn	Lys	Gly	Pro	Trp	Lys	Gln	Glu	Asn	Val	Glu	
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gct	gaa	gct	tcc	atg	gtg	atc	gca	gtc	cca	gag	ccc	ttt	ggg	ggg	gcc	787
Ala	Glu	Ala	Ser	Met	Val	Ile	Ala	Val	Pro	Glu	Pro	Phe	Gly	Gly	Ala	
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Ile Arg Asn Gly Ile Gly Ile His Glu His Ala Ser Ile Asp Leu Pro
390 395 400 405

gat gac act ttg gtg ctc tct ttt gtg ggc cag aca aga gtt ctc atg 1411
Asp Asp Thr Leu Val Leu Ser Phe Val Gly Gln Thr Arg Val Leu Met
425 430 435

gat cag cag act ttc ttc tgt ggc aac gtg gct cat cag cag ctt atc 1507
Asp Gln Gln Thr Phe Phe Cys Gly Asn Val Ala His Gln Gln Leu Ile
455 460 465

ctg gtc agt gaa tgg aag gag cct cag gcc aag aac atc agt gtg gcc 1603
Leu Val Ser Glu Trp Lys Glu Pro Gln Ala Lys Asn Ile Ser Val Ala
490 495 500

tat ctg cag atc cat cct cag gag ctc cgg cag atc agc cac aca gag 1699
Tyr Leu Gln Ile His Pro Gln Glu Leu Arg Gln Ile Ser His Thr Glu
520 525 530

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Asn Gly Leu Ser Pro Leu Cys Ala Ile Gly Leu Trp Thr Asp Ile Ser			
550	555	560	565
gct cgt atc ttg aag ttg ccc tct ttt gaa cta ctg cac aag gag atg			1843
Ala Arg Ile Leu Lys Leu Pro Ser Phe Glu Leu Leu His Lys Glu Met			
	570	575	580
ctg ggt gga gag atc att cct cgc tcc atc ctg atg acc acc ttt gag			1891
Leu Gly Gly Glu Ile Ile Pro Arg Ser Ile Leu Met Thr Thr Phe Glu			
	585	590	595
agt agc cat tac ctc ctt tgt gcc ttg gga gat gga gcg ctt ttc tac			1939
Ser Ser His Tyr Leu Leu Cys Ala Leu Gly Asp Gly Ala Leu Phe Tyr			
	600	605	610
ttt ggg ctc aac att gag aca ggt ctg ttg agc gac cgt aag aag gtg			1987
Phe Gly Leu Asn Ile Glu Thr Gly Leu Leu Ser Asp Arg Lys Lys Val			
	615	620	625
act ttg ggc acc cag ccc acc gta ttg agg act ttt cgt tct ctt tct			2035
Thr Leu Gly Thr Gln Pro Thr Val Leu Arg Thr Phe Arg Ser Leu Ser			
	630	635	640
acc acc aac gtc ttt gct tgt tct gac cgc ccc act gtc atc tat agc			2083
Thr Thr Asn Val Phe Ala Cys Ser Asp Arg Pro Thr Val Ile Tyr Ser			
	650	655	660
agc aac cac aaa ttg gtc ttc tca aat gtc aac ctc aag gaa gtg aac			2131
Ser Asn His Lys Leu Val Phe Ser Asn Val Asn Leu Lys Glu Val Asn			
	665	670	675
tac atg tgt ccc ctc aat tca gat ggc tat cct gac agc ctg gcg ctg			2179
Tyr Met Cys Pro Leu Asn Ser Asp Gly Tyr Pro Asp Ser Leu Ala Leu			
	680	685	690
gcc aac aat agc acc ctc acc att ggc acc atc gat gag atc cag aag			2227

Ala Asn Asn Ser Thr Leu Thr Ile Gly Thr Ile Asp Glu Ile Gln Lys	
695	700 705
ctg cac att cgc aca gtt ccc ctc tat gag tct cca agg aag atc tgc	2275
Leu His Ile Arg Thr Val Pro Leu Tyr Glu Ser Pro Arg Lys Ile Cys	
710	715 720 725
tac cag gaa gtg tcc cag tgt ttc ggg gtc ctc tcc agc cgc att gaa	2323
Tyr Gln Glu Val Ser Gln Cys Phe Gly Val Leu Ser Ser Arg Ile Glu	
	730 735 740
gtc caa gac acg agt ggg ggc acg aca gcc ttg agg ccc agc gct agc	2371
Val Gln Asp Thr Ser Gly Gly Thr Thr Ala Leu Arg Pro Ser Ala Ser	
	745 750 755
acc cag gct ctg tcc agc agt gta agc tcc agc aag ctg ttc tcc agc	2419
Thr Gln Ala Leu Ser Ser Ser Val Ser Ser Ser Lys Leu Phe Ser Ser	
	760 765 770
agc act gct cct cat gag acc tcc ttt gga gaa gag gtg gag gtg cac	2467
Ser Thr Ala Pro His Glu Thr Ser Phe Gly Glu Glu Val Glu Val His	
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aac cta ctt atc att gac caa cac acc ttt gaa gtg ctt cat gcc cac	2515
Asn Leu Leu Ile Ile Asp Gln His Thr Phe Glu Val Leu His Ala His	
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cag ttt ctg cag aat gaa tat gcc ctc agt ctg gtt tcc tgc aag ctg	2563
Gln Phe Leu Gln Asn Glu Tyr Ala Leu Ser Leu Val Ser Cys Lys Leu	
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ggc aaa gac ccc aac act tac ttc att gtg ggc aca gca atg gtg tat	2611
Gly Lys Asp Pro Asn Thr Tyr Phe Ile Val Gly Thr Ala Met Val Tyr	
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cct gaa gag gca gag ccc aag cag ggt cgc att gtg gtc ttt cag tat	2659
Pro Glu Glu Ala Glu Pro Lys Gln Gly Arg Ile Val Val Phe Gln Tyr	
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tcg gat gga aaa cta cag act gtg gct gaa aag gaa gtg aaa ggg gcc	2707
Ser Asp Gly Lys Leu Gln Thr Val Ala Glu Lys Glu Val Lys Gly Ala	
855 860 865	
gtg tac tct atg gtg gaa ttt aac ggg aag ctg tta gcc agc atc aat	2755
Val Tyr Ser Met Val Glu Phe Asn Gly Lys Leu Leu Ala Ser Ile Asn	
870 875 880 885	
agc acg gtg cgg ctc tat gag tgg aca aca gag aag gag ctg cgc act	2803
Ser Thr Val Arg Leu Tyr Glu Trp Thr Thr Glu Lys Glu Leu Arg Thr	
890 895 900	
gag tgc aac cac tac aac aac atc atg gcc ctc tac ctg aag acc aag	2851
Glu Cys Asn His Tyr Asn Asn Ile Met Ala Leu Tyr Leu Lys Thr Lys	
905 910 915	
ggc gac ttc atc ctg gtg ggc gac ctt atg cgc tca gtg ctg ctg ctt	2899
Gly Asp Phe Ile Leu Val Gly Asp Leu Met Arg Ser Val Leu Leu Leu	
920 925 930	
gcc tac aag ccc atg gaa gga aac ttt gaa gag att gct cga gac ttt	2947
Ala Tyr Lys Pro Met Glu Gly Asn Phe Glu Glu Ile Ala Arg Asp Phe	
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aat ccc aac tgg atg agt gct gtg gaa atc ttg gat gat gac aat ttt	2995
Asn Pro Asn Trp Met Ser Ala Val Glu Ile Leu Asp Asp Asp Asn Phe	
950 955 960 965	
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Leu Gly Ala Glu Asn Ala Phe Asn Leu Phe Val Cys Gln Lys Asp Ser	
970 975 980	
gct gcc acc act gac gag gag cgg cag cac ctc cag gag gtt ggt ctt	3091
Ala Ala Thr Thr Asp Glu Glu Arg Gln His Leu Gln Glu Val Gly Leu	
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Phe His Leu Gly Glu Phe Val Asn Val Phe Cys His Gly Ser Leu Val	
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